T1R HETERO-OLIGOMERIC TASTE RECEPTORS

Related Applications

This application is related to US Provisional Application Serial No. 60/280,606 filed April 19, 2001, and claims priority of U.S. Provisional Patent Application entitled "T1R Hetero-Oligomeric Taste Receptors" filed June 26, 2001, the contents of which are herein incorporated by reference in its entirety.

Background of the Invention

Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, to family of such receptors, and to the genes and cDNA encoding said receptors. More particularly, the invention relates to newly identified mammalian chemosensory G protein-coupled receptors active in taste signaling which function as hetero-oligomers.

Description of the Related Art

The taste system provides sensory information about the chemical composition of the external world. Taste transduction is one of the most sophisticated forms of chemical-triggered sensation in animals. At present, the means by which taste sensations are elicited remains poorly understood. *See, e.g.,* Margolskee, *BioEssays*, 15:645-50 (1993); Avenet *et al., J. Membrane Biol.*, 112:1-8 (1989). Taste signaling is found throughout the animal kingdom, from simple metazoans to the most complex of vertebrates. Taste sensation is thought to involve distinct signaling pathways. These pathways are believed to be mediated by receptors, *i.e.*, metabotropic or inotropic receptors. Cells which express taste receptors, when exposed to certain chemical stimuli, elicit taste sensation by depolarizing to generate an action potential, which is believed to trigger the sensation. This event is believed to trigger the release of neurotransmitters at gustatory afferent neuron synapses, thereby initiating signaling along neuronal pathways that mediate taste perception. *See, e.g.,* Roper, *Ann. Rev. Neurosci.*, 12:329-53 (1989).

As such, taste receptors specifically recognize molecules that elicit specific taste sensation. These molecules are also referred to herein as "tastants." Many taste receptors belong to the 7-transmembrane receptor superfamily (Hoon *et al.*, *Cell* 96:451 (1999); Adler *et al.*, *Cell* 100:693 (2000)), which are also known as G protein-coupled receptors (GPCRs). Other tastes are believed to be mediated by channel proteins. G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis, carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). *See, e.g.,* Kawamura *et al.*, *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715-31 (1992); Lindemann, *Physiol. Rev.*, 76:718-66 (1996); Stewart *et al.*, *Am. J. Physiol.*, 272:1-26(1997). Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. *See, e.g.*, Akabas *et al.*, *Science*, 242:1047-50 (1988); Gilbertson *et al.*, *J. Gen. Physiol.*,

100:803-24 (1992); Bernhardt *et al.*, *J. Physiol.*, 490:325-36 (1996); Cummings *et al.*, *J. Neurophysiol.*, 75:1256-63 (1996).

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds to thousands of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, contain dozens to hundreds of taste buds. Further, fungiform papillae, located at the front of the tongue, contain only a single or a few taste buds.

Each taste bud, depending on the species, contains 50-150 cells, including precursor cells, support cells, and taste receptor cells. *See, e.g.*, Lindemann, *Physiol. Rev.*, 76:718-66 (1996). Receptor cells are innervated at their base by afferent nerve endings that transmit information to the taste centers of the cortex through synapses in the brain stem and thalamus. Elucidating the mechanisms of taste cell signaling and information processing is important to understanding the function, regulation, and perception of the sense of taste.

Although much is known about the psychophysics and physiology of taste cell function, very little is known about the molecules and pathways that mediate its sensory signaling response. The identification and isolation of novel taste receptors and taste signaling molecules could allow for new methods of chemical and genetic modulation of taste transduction pathways. For example, the availability of receptor and channel molecules could permit the screening for high affinity agonists, antagonists, inverse agonists, and modulators of taste activity. Such taste modulating compounds could be useful in the pharmaceutical and food industries to improve the taste of a variety of consumer products, or to block undesirable tastes, *e.g.*, in certain pharmaceuticals.

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. *See, e.g.,* Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-977 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999). *See also,* EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Because of the complexity of ligand-receptor interactions, and more particularly tastant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better

understanding of the interactions between chemosensory receptors and chemical stimuli. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such receptors, and the genes a cDNAs encoding such receptors, to identify molecules that can be used to modulate chemosensory transduction, such as taste sensation.

Summary of the Invention

The invention relates to a new family of G protein-coupled receptors, and to the genes and cDNAs encoding said receptors. The receptors are thought to be primarily involved in sweet taste transduction as hetero-oligomeric complexes, but can be involved in transducing signals from other taste modalities as well.

The invention provides methods for identifying putative taste modulating compounds. Preferably, such methods may be performed by using the receptor polypeptides and genes encoding said receptor polypeptides disclosed herein.

Toward that end, it is an object of the invention to provide a new family of mammalian G protein-coupled receptors, herein referred to as T1Rs, active in taste perception as hetero-oligomeric complexes. It is another object of the invention to provide fragments and variants of such T1Rs that retain tastant-binding activity. It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such T1Rs, fragments, or variants thereof.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such T1Rs, or fragments or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequence involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such T1Rs, or fragments or variants thereof.

It is still another object of the invention to provide T1R fusion proteins or polypeptides which include at least a fragment of at least one of such T1Rs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding a T1R polypeptide comprising a nucleic acid sequence that is at least 50%, preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a

nucleic acid sequence selected from the group consisting of: SEQ ID NOS: 1, 3, 5, 7, and conservatively modified variants thereof.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 35 to 50%, and preferably 60%, 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ ID NOS: 2, 4, 6, and conservatively modified variants thereof, wherein the fragment is at least 20, preferably 40, 60, 80, 100, 150, 200, or 250 amino acids in length. Optionally, the fragment can be an antigenic fragment which binds to an anti-T1R antibody.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists or antagonists of such T1Rs, or fragments or variants thereof.

It is still another object of the invention to provide a PDZ-interacting peptide (herein referred to as PDZIP) which can facilitate surface expression of integral plasma membrane proteins, specifically GPCRs. It is also an object of the invention to provide vectors including PDZIP, host cells expressing such vectors, and methods of using PDZIP to facilitate surface expression.

It is yet another object of the invention to provide methods for identifying taste modulating compounds, particularly sweet taste modulating compounds. Preferably, such methods may be performed by using a combination of T1Rs, or fragments or variants thereof, and genes encoding such T1Rs, or fragments or variants thereof, disclosed herein.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of a taste detectable by a mammal, comprising: a step of contacting said one or more compounds with at least one hetero-oligomeric complex of the disclosed T1Rs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a taste, comprising the steps of: for each of a plurality of T1R hetero-oligomers, or

fragments of variants thereof disclosed herein, preferably human T1Rs, ascertaining the extent to which the T1R hetero-oligomer interacts with the tastant; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the T1R hetero-oligomer, in amounts that together provide a receptor-stimulation profile that mimics the profile for the taste. Interaction of a tastant with a T1R hetero-oligomer can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the tastant.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of T1R hetero-oligomers, or fragments or variants thereof, to ascertain the extent to which the T1Rs hetero-oligomers each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the taste.

Brief Description of the Figures

Figure 1A contains the results of an immunofluorescence staining of Myc-tagged hT1R2 which indicates that PDZIP increases expression of hT1R2 on the plasma membrane.

Figures 1B contains FACS analysis data demonstrating that PDZIP increases expression of hT1R2 on the plasma membrane.

Figures 2A through 2L contain calcium imaging data demonstrating hT1R2/hT1R3 responses to sweet stimuli.

Figure 3 contains cDNA expression data showing that hT1R2 and hT1R3 are expressed in human tongue epithelium.

Figures 4A through 4E

~~Figure 4~~ contains fluorescence microscopy data which indicates that hT1R2 and hT1R3 act in combination and bind sweet taste stimuli ligands.

Figure 5 contains normalized dose-response curves the results of which indicate that T1R2 and T1R3 function together as the human sweet taste receptor based on their dose-specific interaction with values sweet stimuli.

Figure 6 presents cyclamate responses for cells expressing hT1R2/hT1R3 and for cells expressing hT1R3.

Figure 7 depicts the glutamate binding site in the x-ray crystal structure of mGluR1.

Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding taste-cell-specific G protein-coupled receptors ("GPCR"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the T1R family of taste-cell-specific GPCRs. Members of the T1R family of taste-cell-specific GPCRs are identified in Hoon *et al.*, *Cell*, 96:541-551 (1999), WO 00/06592, WO 00/06593, and U.S. Serial No. 09/799,629, all of which are incorporated herein by reference in their entireties.

More particularly, the invention provides nucleic acids encoding a novel family of taste-cell-specific GPCRs. These nucleic acids and the receptors that they encode are referred to as members of the "T1R" family of taste-cell-specific GPCRs. In particular embodiments of the invention, the T1R family members include rT1R3, mT1R3, hT1R3, and hT1R1. While not wishing to be bound by theory, it is believed that these taste-cell-specific GPCRs are components of the taste transduction pathway, and may be involved in the taste detection of sweet substances and/or other taste modalities.

Further, it is believed that T1R family members act in combination as hetero-oligomeric complexes with other T1R family members, other taste-cell-specific GPCRs, or a combination thereof, to thereby effect chemosensory taste transduction. For instance, it is believed that T1R2 and T1R3 may be co-expressed within the same

taste receptor cell type, and the two receptors may physically interact to form a heterodimeric taste receptor. Additional receptors may also be co-expressed forming hetero-oligomeric taste receptor with the T1Rs disclosed herein. Alternatively, T1R2 and T1R3 may both independently bind to the same type of ligand, and their combined binding may result in a specific perceived taste sensation.

These nucleic acids provide valuable probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. For example, probes for T1R polypeptides and proteins can be used to identify taste cells present in foliate, circumvallate, and fungiform papillae, as well as taste cells present in the geschmackstreifen, oral cavity, gastrointestinal epithelium, and epiglottis. They may also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centers in the brain. In particular, methods of detecting T1Rs can be used to identify taste cells sensitive to sweet tastants or other specific modalities of tastants. Furthermore, the nucleic acids and the proteins they encode can be used as probes to dissect taste-induced behaviors. Also, chromosome localization of the genes encoding human T1Rs can be used to identify diseases, mutations, and traits caused by and associated with T1R family members.

The nucleic acids encoding the T1R proteins and polypeptides of the invention can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/035374, which is herein incorporated by reference in its entirety.

The invention also provides methods of screening for modulators, *e.g.*, activators, inhibitors, stimulators, enhancers, agonists, and antagonists, of these novel taste-cell-specific GPCRs. Such modulators of taste transduction are useful for pharmacological, chemical, and genetic modulation of taste signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of taste cell activity. These modulatory compounds can then be used in the food and pharmaceutical industries to customize taste, *e.g.*, to modulate the sweet tastes of foods or drugs.

Thus, the invention provides assays for detecting and characterizing taste modulation, wherein T1R family members act as direct or indirect reporter molecules

of the effect of modulators on taste transduction. GPCRs can be used in assays to, *e.g.*, measure changes in ligand binding, ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interactions, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, members of the T1R family can be used as indirect reporters via attachment to a second reporter molecule such as green fluorescent protein (*see*, *e.g.*, Mistili & Spector, *Nature Biotechnology*, 15:961-964 (1997)). In another embodiment, T1R family members may be recombinantly expressed in cells, and modulation of taste transduction via GPCR activity may be assayed by measuring changes in Ca^{2+} levels and other intracellular messages such as cAMP, cGMP, or IP3.

In certain embodiments, a domain of a T1R polypeptide, *e.g.*, an extracellular, transmembrane, or intracellular domain, is fused to a heterologous polypeptide, thereby forming a chimeric polypeptide, *e.g.*, a chimeric polypeptide with GPCR activity. Such chimeric polypeptides are useful, *e.g.*, in assays to identify ligands, agonists, antagonists, or other modulators of a T1R polypeptide. In addition, such chimeric polypeptides are useful to create novel taste receptors with novel ligand binding specificity, modes of regulation, signal transduction pathways, or other such properties, or to create novel taste receptors with novel combinations of ligand binding specificity, modes of regulation, signal transduction pathways, *etc.*

In one embodiment, a T1R polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates plasma membrane trafficking, or maturation and targeting through the secretory pathway. The optional heterologous sequence may be a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Alternatively, the optional heterologous sequence may be a PDZ-interacting peptide, such as a C-terminal PDZIP fragment (SEQ ID NO 10). PDZIP is an ER export signal which, according to the present invention, has been shown to facilitate surface expression of heterologous proteins such as the T1R receptors described herein. More particularly, in one aspect of the invention, PDZIP can be used to promote proper targeting of problematic membrane proteins such as olfactory receptors, T2R taste receptors, and the T1R taste receptors described herein.

Such chimeric T1R receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a G protein, *e.g.*, Gα15 or Gα16 or

another type of promiscuous G protein capable of pairing a wide range of chemosensory GPCRs to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell. If preferred host cells do not express an appropriate G protein, they may be transfected with a gene encoding a promiscuous G protein such as those described in US Application Serial No. 60/243,770, which is herein incorporated by reference in its entirety.

Methods of assaying for modulators of taste transduction include *in vitro* ligand-binding assays using: T1R polypeptides, portions thereof, *i.e.*, the extracellular domain, transmembrane region, or combinations thereof, or chimeric proteins comprising one or more domains of a T1R family member; oocyte or tissue culture cells expressing T1R polypeptides, fragments, or fusion proteins; phosphorylation and dephosphorylation of T1R family members; G protein binding to GPCRs; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cGMP, CAMP and inositol triphosphate (IP3); changes in intracellular calcium levels; and neurotransmitter release.

Further, the invention provides methods of detecting T1R nucleic acid and protein expression, allowing investigation of taste transduction regulation and specific identification of taste receptor cells. T1R family members also provide useful nucleic acid probes for paternity and forensic investigations. T1R genes are also useful as nucleic acid probes for identifying taste receptor cells, such as foliate, fungiform, circumvallate, geschmackstreifen, and epiglottis taste receptor cells. T1R receptors can also be used to generate monoclonal and polyclonal antibodies useful for identifying taste receptor cells. Taste receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A+ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

Functionally, the T1R polypeptides comprise a family of related seven transmembrane G protein-coupled receptors, which are believed to be involved in taste transduction and may interact with a G protein to mediate taste signal

transduction as hetero-oligomeric complexes (*see, e.g.*, Fong, *Cell Signal*, 8:217 (1996); Baldwin, *Curr. Opin. Cell Biol.*, 6:180 (1994)). Structurally, the nucleotide sequences of T1R family members may encode related polypeptides comprising an extracellular domain, seven transmembrane domains, and a cytoplasmic domain. Related T1R family genes from other species share at least about 50%, and optionally 60%, 70%, 80%, or 90%, nucleotide sequence identity over a region of at least about 50 nucleotides in length, optionally 100, 200, 500, or more nucleotides in length to SEQ ID NOS 1, 3, 5, 7, or conservatively modified variants thereof, or encode polypeptides sharing at least about 35 to 50%, and optionally 60%, 70%, 80%, or 90%, amino acid sequence identity over an amino acid region at least about 25 amino acids in length, optionally 50 to 100 amino acids in length to SEQ ID NOS: 2, 4, 6, or conservatively modified variants thereof.

Several consensus amino acid sequences or domains have also been identified that are characteristic of T1R family members. For example, T1R family members typically comprise a sequence having at least about 50%, optionally 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95-99%, or higher, identity to T1R consensus sequences 1 and 2 (SEQ ID NOs 8 and 9, respectively). These conserved domains thus can be used to identify members of the T1R family, by identity, specific hybridization or amplification, or specific binding by antibodies raised against a domain. Such T1R consensus sequences have the following amino acid sequences:

T1R Family Consensus Sequence 1: (SEQ ID NO: 8)

(TR)C(FL)(RQP)R(RT)(SPV)(VERKT)FL(AE)(WL)(RHG)E

T1R Family Consensus Sequence 2: (SEQ ID NO: 9)

(LQ)P(EGT)(NRC)YN(RE)A(RK)(CGF)(VLI)T(FL)(AS)(ML)

These consensus sequences are inclusive of those found in the T1R polypeptides described herein, but T1R family members from other organisms may be expected to comprise consensus sequences having about 75% identity or more to the inclusive consensus sequences described specifically herein.

Specific regions of the T1R nucleotide and amino acid sequences may be used to identify polymorphic variants, interspecies homologs, and alleles of T1R family members. This identification can be made *in vitro*, *e.g.*, under stringent hybridization conditions or PCR (*e.g.*, using primers encoding the T1R consensus sequences

identified above), or by using the sequence information in a computer system for comparison with other nucleotide sequences. Different alleles of T1R genes within a single species population will also be useful in determining whether differences in allelic sequences correlate to differences in taste perception between members of the population. Classical PCR-type amplification and cloning techniques are useful for isolating orthologs, for example, where degenerate primers are sufficient for detecting related genes across species, which typically have a higher level of relative identity than paralogous members of the T1R family within a single species.

Typically, identification of polymorphic variants and alleles of T1R family members can be made by comparing an amino acid sequence of about 25 amino acids or more, *e.g.*, 50-100 amino acids. Amino acid identity of approximately at least 35 to 50%, and optionally 60%, 70%, 75%, 80%, 85%, 90%, 95-99%, or above typically demonstrates that a protein is a polymorphic variant, interspecies homolog, or allele of a T1R family member. Sequence comparison can be performed using any of the sequence comparison algorithms discussed below. Antibodies that bind specifically to T1R polypeptides or a conserved region thereof can also be used to identify alleles, interspecies homologs, and polymorphic variants.

Polymorphic variants, interspecies homologs, and alleles of T1R genes can be confirmed by examining taste-cell-specific expression of the putative T1R polypeptide. Typically, T1R polypeptides having an amino acid sequence disclosed herein can be used as a positive control in comparison to the putative T1R polypeptide to demonstrate the identification of a polymorphic variant or allele of the T1R family member. The polymorphic variants, alleles, and interspecies homologs are expected to retain the seven transmembrane structure of a G protein-coupled receptor. For further detail, *see* WO 00/06592, which discloses related T1R family members, GPCR-B3s, the contents of which are herein incorporated by reference in a manner consistent with this disclosure. GPCR-B3 receptors are referred to herein as rT1R1 and mT1R1. Additionally, *see* WO 00/06593, which also discloses related T1R family members, GPCR-B4s, the contents of which are herein incorporated by reference in a manner consistent with this disclosure. GPCR-B4 receptors are referred to herein as rT1R2 and mT1R2.

Nucleotide and amino acid sequence information for T1R family members may also be used to construct models of taste-cell-specific polypeptides in a computer system. These models can be subsequently used to identify compounds that can activate or inhibit T1R receptor proteins. Such compounds that modulate the activity of T1R family members can then be used to investigate the role of T1R genes and receptors in taste transduction.

The present invention also provides assays, preferably high throughput assays, to identify molecules that interact with and/or modulate T1R polypeptide hetero-oligomeric complexes. In numerous assays, a particular domain of a T1R family member is used in combination with a particular domain of another T1R family member, *e.g.*, an extracellular, transmembrane, or intracellular domain or region. In numerous embodiments, an extracellular domain, transmembrane region or combination thereof may be bound to a solid substrate, and used, *e.g.*, to isolate ligands, agonists, antagonists, or any other molecules that can bind to and/or modulate the activity of a T1R polypeptide.

While not wishing to be bound to any particular theory, the T1R family of receptors is predicted to be involved in sweet taste transduction by virtue of the linkage of mTIR3 to the *Sac* locus, a locus on the distal end of chromosome four that influences sweet taste. Human T1R3 has also been reported to localize to 1p36.2-1p36.33, a region that displays conserved synteny with the mouse interval containing *Sac* and T1R1. Further hetero-oligomeric complexes of T1R family members have been shown to respond to sweet taste stimuli. However, T1R type receptors may mediate other taste modalities, such as bitter, umami, sour and salty.

Various conservative mutations and substitutions are envisioned to be within the scope of the invention. For instance, it would be within the level of skill in the art to perform amino acid substitutions using known protocols of recombinant gene technology including PCR, gene cloning, site-directed mutagenesis of cDNA, transfection of host cells, and in-vitro transcription. The variants could then be screened for taste-cell-specific GPCR functional activity.

A. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

"Taste cells" include neuroepithelial cells that are organized into groups to form taste buds of the tongue, *e.g.*, foliate, fungiform, and circumvallate cells (*see*, *e.g.*, Roper et al., Ann. Rev. Neurosci. 12:329-353 (1989)). Taste cells are also found in the palate and other tissues, such as the esophagus and the stomach.

"T1R" refers to one or more members of a family of G protein-coupled receptors that are expressed in taste cells such as foliate, fungiform, and circumvallate cells, as well as cells of the palate, and esophagus (*see*, *e.g.*, Hoon *et al.*, *Cell*, 96:541-551 (1999), herein incorporated by reference in its entirety). Members of this family are also referred to as GPCR-B3 and TR1 in WO 00/06592 as well as GPCR-B4 and TR2 in WO 00/06593. GPCR-B3 is also herein referred to as rT1R1, and GPCR-B4 is referred to as rT1R2. Taste receptor cells can also be identified on the basis of morphology (*see*, *e.g.*, Roper, *supra*), or by the expression of proteins specifically expressed in taste cells. T1R family members may have the ability to act as receptors for sweet taste transduction, or to distinguish between various other taste modalities.

"T1R" nucleic acids encode a family of GPCRs with seven transmembrane regions that have "G protein-coupled receptor activity," *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP3, cAMP, cGMP, and Ca^{2+} via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see*, *e.g.*, Fong, *supra*, and Baldwin, *supra*). A single taste cell may contain many distinct T1R polypeptides.

The term "T1R" family therefore refers to polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have at least about 35 to 50% amino acid sequence identity, optionally about 60, 75, 80, 85, 90, 95, 96, 97, 98, or 99% amino acid sequence identity to SEQ ID NOS: 2, 4, or 6 over a window of about 25 amino acids, optionally 50-100 amino acids; (2) specifically bind to antibodies raised against an immunogen comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, and conservatively modified variants thereof; (3) are encoded by a nucleic acid molecule which specifically hybridize (with a size of at least about 100, optionally at least about 500-1000 nucleotides) under stringent hybridization conditions to a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5,

7, and conservatively modified variants thereof; or (4) comprise a sequence at least about 35 to 50% identical to an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, and 6.

Topologically, certain chemosensory GPCRs have an "N-terminal domain;" "extracellular domains;" "transmembrane domains" comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; "cytoplasmic domains," and a "C-terminal domain" (*see, e.g.*, Hoon *et al., Cell*, 96:541-551 (1999); Buck & Axel, *Cell*, 65:175-187 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g.*, Stryer, *Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand-binding assays.

"Extracellular domains" therefore refers to the domains of T1R polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the "N terminal domain" that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The "N-terminal domain" region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. More particularly, in one embodiment of the invention, this domain starts at the N-terminus and ends approximately at the conserved glutamic acid at amino acid position 563 plus or minus approximately 20 amino acid. These extracellular domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase. In addition, transmembrane regions, described below, can also bind ligand either in combination with the extracellular domain, and are therefore also useful for *in vitro* ligand-binding assays.

"Transmembrane domain," which comprises the seven "transmembrane regions," refers to the domain of T1R polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and

extracellular loops. In one embodiment, this region corresponds to the domain of T1R family members which starts approximately at the conserved glutamic acid residue at amino acid position 563 plus or minus 20 amino acids and ends approximately at the conserved tyrosine amino acid residue at position 812 plus or minus approximately 10 amino acids. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*.

"Cytoplasmic domains" refers to the domains of T1R polypeptides that face the inside of the cell, *e.g.*, the "C-terminal domain" and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. "C-terminal domain" refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm. In one embodiment, this region starts at the conserved tyrosine amino acid residue at position 812 plus or minus approximately 10 amino acids and continues to the C-terminus of the polypeptide.

The term "ligand-binding region" or "ligand-binding domain" refers to sequences derived from a chemosensory receptor, particularly a taste receptor, that substantially incorporates at least the extracellular domain of the receptor. In one embodiment, the extracellular domain of the ligand-binding region may include the N-terminal domain and, optionally, portions of the transmembrane domain, such as the extracellular loops of the transmembrane domain. The ligand-binding region may be capable of binding a ligand, and more particularly, a tastant.

The phrase "hetero-oligomer" or "hetero-oligomeric complex" in the context of the T1R receptors or polypeptides of the invention refers to a functional combination of at least two T1R receptors or polypeptides, at least one T1R receptor or polypeptide and another taste-cell-specific GPCRs, or a combination thereof, to thereby effect chemosensory taste transduction. For instance, the receptors or polypeptides may be co-expressed within the same taste receptor cell type, and the two receptors may physically interact to form a hetero-oligomeric taste receptor. Alternatively, the receptors or polypeptides may both independently bind to the same

type of ligand, and their combined binding may result in a specific perceived taste sensation.

The phrase "functional effects" in the context of assays for testing compounds that modulate T1R family member mediated taste transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP3, or intracellular Ca^{2+}), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a T1R family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte T1R gene expression; tissue culture cell T1R expression; transcriptional activation of T1R genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

"Inhibitors," "activators," and "modulators" of T1R genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for taste transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate taste transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate taste transduction, *e.g.*,

agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of T1R family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing T1R family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on taste transduction, as described above. Samples or assays comprising T1R family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative T1R activity value of 100%. Inhibition of a T1R is achieved when the T1R activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of a T1R is achieved when the T1R activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or

compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g.*, *Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); Antisense Strategies, *Annals of the N.Y. Academy of Sciences*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide, a 7-transmembrane receptor. However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (*e.g.*, a taste receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, as with the T1R receptors of the present invention, the use of other translocation domains may be preferred. For instance, a PDZ-interacting peptide, as described herein, may be used.

The "translocation domain," "ligand-binding domain", and chimeric receptors compositions described herein also include "analogs," or "conservative variants" and "mimetics" ("peptidomimetics") with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity.

More particularly, "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the

degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.*, Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of Protein Structure*, Springer-Vrlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a

single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH_2- for -C(=O)-NH-), aminomethylene (CH_2-NH), ethylene, olefin (CH=CH), ether (CH_2-O), thioether (CH_2-S), tetrazole (CN_4), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic

by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, *e.g.*, by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is

typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60° C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, Sx SSC, and 1% SDS, incubating at 42°C, or, Sx SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides which they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCI, 1% SDS at 37°C, and a wash in 1X SSC at

45°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60, or more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

An "anti-T1R" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a T1R gene, cDNA, or a subsequence thereof.

The term "immunoassay" is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase "specifically (or selectively) binds" to an antibody or, "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a

heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a T1R family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the T1R polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the T1R polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with T1R molecules from other species or other T1R molecules. Antibodies can also be selected that recognize only T1R GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g.*, Harlow & Lane, *Antibodies, A Laboratory Manual*, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as E. toll, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.*, cultured cells, explants, and cells *in vivo*.

B. Isolation and Expression of T1R Polypeptides

Isolation and expression of the T1Rs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding taste receptor ligand-binding regions, and libraries of these nucleic acids can optionally be generated. Individual expression vectors or libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these nucleic acids or libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect, or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may

then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature. *See, e.g.*, Sambrook, ed., Molecular Cloning: a Laboratory manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); Current Protocols in Molecular Biology, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.*, analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, *e.g.*, fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.*, SDS-PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers may be used to amplify nucleic acid fragments encoding taste receptor ligand-binding regions. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Amplification methods are also well known in the art, and include, *e.g.*, polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, N.Y. (1990) and *PCR Strategies*, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (*see, e.g.*, Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (*see, e.g.*, Kwoh, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)); and, self-

sustained sequence replication (*see, e.g.*, Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874 (1990)); Q Beta replicase amplification (*see, e.g.*, Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (*see, e.g.*, Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (*e.g.*, NASBA, Cangene, Mississauga, Ontario); *see also* Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor. Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like). Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039.

The primer pairs may be designed to selectively amplify ligand-binding regions of the T1R family members. These regions may vary for different ligands or tastants. Thus, what may be a minimal binding region for one tastant, may be too limiting for a second tastant. Accordingly, ligand-binding regions of different sizes comprising different extracellular domain structures may be amplified.

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as http://blocks.fhcrc.org/codehop.html, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known taste receptor ligand-binding regions (*see, e.g.*, Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques* 24:318-319 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial

nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g.*, Hoops, *Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g.*, Morales, *Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g.*, Hill, *Proc. Natl. Acad. Sci. USA* 95:4258-4263 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a taste receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to clone T1R polypeptides and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a T1R polypeptide, which also recognize and selectively bind to the T1R homolog.

Nucleic acids that encode ligand-binding regions of taste receptors may be generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from taste receptor-expressing cells.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids encoding T1Rs fused to translocation sequences may be constructed. Also provided are hybrid T1Rs comprising the translocation motifs and tastant-binding domains of other families of chemosensory receptors, particularly taste receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and

enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, and transgenics, a promoter fragment can be employed to direct expression of the desired nucleic acid in all desired cells or tissues.

In another embodiment, fusion proteins may include C-terminal or N-terminal translocation sequences. Further, fusion proteins can comprise additional elements, *e.g.*, for protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts, histidine-tryptophan modules, or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.*, Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.*, Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide encoding a nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.*, Williams, *Biochemistry* 34:1787-1797 (1995)), and an C-terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g.*, Kroll, *DNA Cell. Biol.* 12:441-53 (1993).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the ligand-binding domain encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g.*, Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider,

Protein Expr. Purif. 6435:10 (1995); Sambrook; Tijssen; Ausubel. Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.*, episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.*, chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.*, chlorosulfuron or Basta) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g.*, Blondelet-Rouault, *Gene* 190:315-317 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992-997 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a T1R ligand-binding domain within any 7-transmembrane polypeptide. Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (*e.g.*, extracellular domain, TM domains, cytoplasmic domain, *etc.*) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. Periodicity detection enhancement and alpha helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Kyte & Doolittle, *J. Md. Bio.*, 157:105-132 (1982); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); http://bioinfo.weizmann.ac.il/.

The present invention also includes not only the DNA and proteins having the specified nucleic and amino acid sequences, but also DNA fragments, particularly fragments of, *e.g.*, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, *e.g.*, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more. Optionally, the nucleic acid fragments can encode an antigenic polypeptide which is capable of binding to an antibody raised against a T1R family member. Further, a protein fragment of the invention can optionally be an antigenic fragment which is capable of binding to an antibody raised against a T1R family member.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the T1R polypeptides described herein, coupled to additional amino acids representing all or part of another GPCR, preferably a member of the 7 transmembrane superfamily. These chimeras can be made from the instant receptors and another GPCR, or they can be made by combining two or more of the present receptors. In one embodiment, one portion of the chimera corresponds tom or is derived from the extracellular domain of a T1R polypeptide of the invention. In another embodiment, one portion of the chimera corresponds to, or is derived from the extracellular domain and one or more of the transmembrane domains of a T1R polypeptide described herein, and the remaining portion or portions can come from another GPCR. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, a taste selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain, a transmembrane domain, a cytoplasmic domain, an N-terminal domain, a C-terminal domain, or any combination thereof, can be covalently linked to a heterologous protein. For instance, an T1R extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a T1R transmembrane

domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β-gal, glutamtate receptor, and the rhodopsin presequence.

Also within the scope of the invention are host cells for expressing the T1Rs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the T1Rs, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at lest one nucleic acid molecule into the host cell capable of expressing the T1R, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

C. <u>**Detection of T1R polypeptides**</u>

In addition to the detection of T1R genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect T1Rs, *e.g.*, to identify taste receptor cells, and variants of T1R family members. Immunoassays can be used to qualitatively or quantitatively analyze the T1Rs. A general overview of the applicable technology can be found in Harlow & Lane, Antibodies: A Laboratory Manual (1988).

1. Antibodies to T1R family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a T1R family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, supra; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-497 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275-1281 (1989); Ward *et al.*, *Nature*, 341:544-546 (1989)).

A number of T1R-comprising immunogens may be used to produce antibodies specifically reactive with a T1R family member. For example, a recombinant T1R polypeptide, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the consensus sequences that are used to identify members of the T1R family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits is immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the T1R. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see* Harlow & Lane, *supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see* Kohler & Milstein, *Eur. J. Immunol.*, 6:511-519 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 104 or greater are selected and tested for their cross reactivity against non-T1R polypeptides, or even other T1R family members or other related proteins from other organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a Kd of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 p.M or better, and optionally 0.01 pM or better.

Once T1R family member specific antibodies are available, individual T1R proteins and protein fragments can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. <u>Immunological binding assays</u>

T1R proteins, fragments, and variants can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see*, *e.g.*, U.S.

Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see also Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a T1R family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-T1R) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled T1R polypeptide or a labeled anti-T1R antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/T1R complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g.*, Kronval *et al.*, *J. Immunol.*, 111:1401-1406 (1973); *Akerstrom et al.*, *J. Immunol.*, 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a T1R polypeptide in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-T1R antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the T1R polypeptide present in the test sample. The T1R polypeptide is thus immobilized is then bound by a labeling agent, such as a second T1R antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of T1R polypeptide present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) T1R polypeptide displaced (competed away) from an anti-T1R antibody by the unknown T1R polypeptide present in a sample. In one competitive assay, a known amount of T1R polypeptide is added to a sample and the sample is then contacted with an antibody that specifically binds to the T1R. The amount of exogenous T1R polypeptide bound to the antibody is inversely proportional to the concentration of T1R polypeptide present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of T1R polypeptide bound to the antibody may be determined either by measuring the amount of T1R polypeptide present in a T1R/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of T1R polypeptide may be detected by providing a labeled T1R molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known T1R polypeptide is immobilized on a solid substrate. A known amount of anti-T1R antibody is added to the sample, and the sample is then contacted with the immobilized T1R. The amount of anti-T1R antibody bound to the known immobilized T1R polypeptide is inversely proportional to the amount of T1R

polypeptide present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. **Cross-reactivity determinations**

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, T1R polypeptides and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the T1R polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the T1R family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a T1R family member, to the immunogen protein (*i.e.*, T1R polypeptide encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a T1R immunogen.

Antibodies raised against T1R conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the T1R family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the T1R family can be made by subtracting out cross-reactive antibodies using other T1R family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T1R1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat T1R1 or mouse T1R1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of T1R polypeptide in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the T1R polypeptide. The anti-T1R polypeptide antibodies specifically bind to the T1R polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-T1R antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see* Monroe *et al.*, *Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions

such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical, or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADSTM), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, 3H, 1251, 3sS, 14C, or ^{32}P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a T1R polypeptide, or secondary antibodies that recognize anti-T1R.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include

fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge-coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

D. Detection of Modulators

Compositions and methods for determining whether a test compound specifically binds to a hetero-oligomeric chemosensory receptor complex of the invention, both *in vitro* and *in vivo*, are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand binding to a T1R polypeptide of the invention. These assays may be performed on intact cells expressing a chemosensory receptor, on permeabilized cells, or on membrane fractions produced by standard methods.

Taste receptors bind tastants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples

are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The T1R proteins or polypeptides of the assay will typically be selected from a polypeptide having a sequence of SEQ ID NOS: 2, 4, 6, or fragments or conservatively modified variants thereof. Optionally, the fragments and variants can be antigenic fragments and variants which bind to an anti-T1R antibody.

Alternatively, the T1R proteins or polypeptides of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having amino acid sequence identity to SEQ ID NOS: 2, 4, 6, or fragments or conservatively modified variants thereof. Generally, the amino acid sequence identity will be at least 35 to 50%, or optionally 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the T1R proteins or polypeptides of the assays can comprise a domain of a T1R protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, and the like. Further, as described above, the T1R protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of T1R receptor activity are tested using T1R proteins or polypeptides as described above, either recombinant or naturally occurring. The T1R proteins or polypeptides can be isolated, co-expressed in a cell, co-expressed in a membrane derived from a cell, co-expressed in tissue or in an animal, either recombinant or naturally occurring. For example, tongue slices, dissociated cells from a tongue, transformed cells, or membranes can be used. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. ***In vitro* binding assays**

Taste transduction can also be examined *in vitro* with soluble or solid state reactions, using hetero-oligomeric complexes of the T1R polypeptides of the invention. In a particular embodiment, hetero-oligomeric complexes of T1R ligand-binding domains can be used *in vitro* in soluble or solid state reactions to assay for ligand binding.

For instance, the T1R N-terminal domain is predicted to be involved in ligand binding. More particularly, the T1Rs belong to a GPCR sub-family that is characterized by large, approximately 600 amino acid, extracellular N-terminal segments. These N-terminal segments are thought to form, at least in part, the ligand-binding domains, and are therefore useful in biochemical assays to identify T1R agonists and antagonists. The ligand-binding domain may also contain additional portions of the extracellular domain, such as the extracellular loops of the transmembrane domain. Similar assays have been used with other GPCRs that are related to the T1Rs, such as the metabotropic glutamate receptors (*see, e.g.,* Han and Hampson, *J. Biol. Chem.* 274:10008-10013 (1999)). These assays might involve displacing a radioactively or fluorescently labeled ligand, measuring changes in intrinsic fluorescence or changes in proteolytic susceptibility, *etc.*

Ligand binding to a hetero-oligomeric complex of T1R polypeptides of the invention can be tested in solution, in a bilayer membrane, optionally attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Preferred binding assays of the invention are biochemical binding assays that use recombinant soluble N-terminal T1R domains.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor complex, or its release from the receptor complex can be examined. More particularly, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins.

In another embodiment of the invention, a GTPγ^{35}S assay may be used. As described above, upon activation of a GPCR, the Gα subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively labeled GTPγ^{35}S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTPγ^{35}S are added to the assay, and binding of GTPγ^{35}S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently labeled GTPγ^{35}S can be utilized.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor ligand binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of ligands to the T1R polypeptides of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small

molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor tastant-binding which may activate or inhibit the chemosensory receptors of the invention, fluorescence-labeled tastants or auto-fluorescent tastants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\amalg} - Int_{\perp}}{Int_{\amalg} + Int_{\perp}}$$

Where $\prod$ is the intensity of the emission light parallel to the excitation light plane and Int $\perp$ is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000 ™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit =1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5° Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\,\mathrm{Re}laxationTime = \frac{3\eta V}{RT}$$

The rotational relaxation time is small ($\approx$ 1 nanosecond) for small molecules (*e.g.* fluorescein) and large ($\approx$ 100 nanoseconds) for large molecules (*e.g.* immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. **Solid state and soluble high throughput assays**

In yet another embodiment, the invention provides soluble assays using a hetero-oligomeric T1R polypeptide complex; or a cell or tissue co-expressing T1R polypeptides. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the T1R polypeptides, or cell or tissue expressing the T1R polypeptides is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non-covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin

are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by

exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.*, Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963) (describing solid phase synthesis of, *e.g.*, peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-274 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al., Science*, 251:767-777 (1991); *Sheldon et al., Clinical Chemistry*, 39(4):718-719 (1993); and Kozal *et al., Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Cell-based binding assays

In one embodiment, a T1R proteins or polypeptides are co-expressed in a eukaryotic cell as chimeric receptors with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. Such chimeric T1R polypeptides can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, Gα15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of 32P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration a taste

receptor stays active would be useful as a means of prolonging a desired taste or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g.*, *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

T1R modulation may be assayed by comparing the response of T1R polypeptides treated with a putative T1R modulator to the response of an untreated control sample. Such putative T1R modulators can include tastants that either inhibit or activate T1R polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative T1R activity value of 100. Inhibition of a T1R polypeptide is achieved when the T1R activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a T1R polypeptide is achieved when the T1R activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in ionic polarization (*i.e.*, electrical potential) of the cell or membrane expressing a T1R polypeptide. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques (*see, e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode, *e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergarrd-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional

consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+}, IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein-coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G protein-coupled receptors, promiscuous G proteins such as Gα15 and Gα16 can be used in the assay of choice (Wilkie *et al.*, *Proc. Nat'l Acad. Sci.*, 88:10049-10053 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP3, which releases intracellular stores of calcium ions. Activation of some G protein-coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3 can be used to assess G protein-coupled receptor function. Cells expressing such G protein-coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP

or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *Proc. Nat'l Acad. Sci.*, 88:9868-9872 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-crated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, T1R polypeptide activity is measured by co-expressing T1R genes in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express T1R genes) and the promiscuous G protein is Gα15 (Offermanns & Simon, *supra*). Modulation of taste transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the T1R signal transduction pathway via administration of a molecule that associates with T1R polypeptides. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the

assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing T1R polypeptides of interest is contacted with a test compound for a sufficient time to effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.*, Mistili & Spector, *Nature Biotechnology*, 15:961-964 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the T1R polypeptide of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the T1R polypeptides of interest.

5. Transgenic non-human animals expressing chemosensory receptors

Non-human animals expressing one or more chemosensory receptor sequences of the invention, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian taste transmembrane receptor complex *in vivo* by contacting a non-human animal stably or transiently transfected with nucleic acids encoding chemosensory receptors or ligand-binding regions thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide complex.

Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize tastants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing human chemosensory receptor sequences can be used for *in vivo* screening of tastants and their effect on, *e.g.*, cell physiology (*e.g.*, on taste neurons), on the CNS, or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ, or whole animal parameters can be measured by a variety of means. The T1R sequences of the invention can be for example co-expressed in animal taste tissues by delivery with an infecting agent, *e.g.*, adenovirus expression vector.

The endogenous chemosensory receptor genes can remain functional and wild-type (native) activity can still be present. In other situations, where it is desirable that all chemosensory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.*,

Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g.*, *see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acids of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat T1R gene sequences can replace the orthologous T1R in the mouse genome. In this way, a mouse expressing a human or rat T1R is produced. This mouse can then be used to analyze the function of human or rat T1Rs, and to identify ligands for such T1Rs.

E. Modulators

The compounds tested as modulators of a T1R family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a T1R gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (*e.g.*, in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma

(St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-493 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.*, 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303

(1993)), peptidyl phosphonates (Campbell *et al., J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al., Nature Biotechnology*, 14(3):309-314 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al., Science*, 274:1520-1522 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

In one aspect of the invention, the T1R modulators can be used in any food product, confectionery, pharmaceutical composition, or ingredient thereof to thereby modulate the taste of the product, composition, or ingredient in a desired manner. For instance, T1R modulators which enhance sweet taste sensation can be added to sweeten a product or composition, while T1R modulators which block undesirable taste sensations can be added to improve the taste of a product or composition.

F. <u>Methods for Representing and Predicting the Perception of Taste</u>

The invention also preferably provides methods for representing the perception of taste and/or for predicting the perception of taste in a mammal, including in a human. Preferably, such methods may be performed by using the receptors and genes encoding said T1R polypeptides disclosed herein.

In one embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined taste perception in a mammal by determining a value of taste perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of taste perception in a mammal for one or more unknown molecules or combinations of molecules as described

above; comparing the value of taste perception in a mammal for one or more unknown compositions to the value of taste perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined taste perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined taste perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined taste perception in a mammal.

In another embodiment of the invention, there is provided a method for simulating a taste, comprising the steps of: for each of a plurality of cloned chemosensory receptors, preferably human receptors, ascertaining the extent to which the receptors interact with the tastant; and combining a plurality of compounds, each having a previously-ascertained interaction with the receptors in amounts that together provide a receptor-stimulation profile that mimics the profile for the tastant. Interaction of a tastant with a chemosensory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 75%, 80%, or 90% of the receptors that are substantially stimulated by the tastant.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of chemosensory receptors to ascertain the extent to which the receptors interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the taste.

G. Kits

T1R genes and their homologs are useful tools for identifying chemosensory receptor cells, for forensics and paternity determinations, and for examining taste transduction. T1R family member-specific reagents that specifically hybridize to T1R nucleic acids, such as T1R probes and primers, and T1R specific reagents that specifically bind to a T1R polypeptide, *e.g.*, T1R antibodies are used to examine taste cell expression and taste transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for a T1R family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a T1R polypeptide can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant T1R polypeptide) and a negative control.

The present invention also provides for kits for screening for modulators of T1R family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: T1R nucleic acids or proteins, reaction tubes, and instructions for testing T1R activity. Optionally, the kit contains a biologically active T1R receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

EXAMPLES

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented

herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

EXAMPLE 1 – hT1R1

The human ortholog (Database accession no. AL159177) of a rat taste receptor, designated rT1R1, is provided below as SEQ ID NO 1. The nucleotide and conceptually translated hT1R1 sequence is also described herein as SEQ ID NO 2.

hT1R1 predicted cds (SEQ ID NO 1)

ATGCTGCTCTGCACGGCTCGCCTGGTCGGCCTGCAGCTTCTCATTTCCTGCTGCTGGGCCTT
TGCCTGCCATAGCACGGAGTCTTCTCCTGACTTCACCCTCCCCGGAGATTACCTCCTGGCA
GGCCTGTTCCCTCTCCATTCTGGCTGTCTGCAGGTGAGGCACAGACCCGAGGTGACCCTGT
GTGACAGGTCTTGTAGCTTCAATGAGCATGGCTACCACCTCTTCCAGGCTATGCGGCTTGG
GGTTGAGGAGATAAACAACTCCACGGCCCTGCTGCCCAACATCACCCTGGGGTACCAGCT
GTATGATGTGTGTTCTGACTCTGCCAATGTGTATGCCACGCTGAGAGTGCTCTCCCTGCCA
GGGCAACACCACATAGAGCTCCAAGGAGACCTTCTCCACTATTCCCCTACGGTGCTGGCAG
TGATTGGGCCTGACAGCACCAACCGTGCTGCCACCACAGCCGCCCTGCTGAGCCCTTTCCT
GGTGCCCATGATTAGCTATGCGGCCAGCAGCGAGACGCTCAGCGTGAAGCGGCAGTATCC
CTCTTTCCTGCGCACCATCCCCAATGACAAGTACCAGGTGGAGACCATGGTGCTGCTGCTG
CAGAAGTTCGGGTGGACCTGGATCTCTCTGGTTGGCAGCAGTGACGACTATGGGCAGCTA
GGGGTGCAGGCACTGGAGAACCAGGCCACTGGTCAGGGGATCTGCATTGCTTTCAAGGAC
ATCATGCCCTTCTCTGCCCAGGTGGGCGATGAGAGGATGCAGTGCCTCATGCGCCACCTGG
CCCAGGCCGGGGCCACCGTCGTGGTTGTTTTTTCCAGCCGGCAGTTGGCCAGGGTGTTTTT
CGAGTCCGTGGTGCTGACCAACCTGACTGGCAAGGTGTGGGTCGCCTCAGAAGCCTGGGC
CCTCTCCAGGCACATCACTGGGGTGCCCGGGATCCAGCGCATTGGGATGGTGCTGGGCGT
GGCCATCCAGAAGAGGGCTGTCCCTGGCCTGAAGGCGTTTGAAGAAGCCTATGCCCGGGC
AGACAAGAAGGCCCCTAGGCCTTGCCACAAGGGCTCCTGGTGCAGCAGCAATCAGCTCTG
CAGAGAATGCCAAGCTTTCATGGCACACACGATGCCCAAGCTCAAAGCCTTCTCCATGAGT
TCTGCCTACAACGCATACCGGGCTGTGTATGCGGTGGCCCATGGCCTCCACCAGCTCCTGG
GCTGTGCCTCTGGAGCTTGTTCCAGGGGCCGAGTCTACCCCTGGCAGCTTTTGGAGCAGAT
CCACAAGGTGCATTTCCTTCTACACAAGGACACTGTGGCGTTTAATGACAACAGAGATCCC
CTCAGTAGCTATAACATAATTGCCTGGGACTGGAATGGACCCAAGTGGACCTTCACGGTCC
TCGGTTCCTCCACATGGTCTCCAGTTCAGCTAAACATAAATGAGACCAAAATCCAGTGGCA
CGGAAAGGACAACCAGGTGCCTAAGTCTGTGTGTTCCAGCGACTGTCTTGAAGGGCACCA
GCGAGTGGTTACGGGTTTCCATCACTGCTGCTTTGAGTGTGTGCCCTGTGGGGCTGGGACC
TTCCTCAACAAGAGTGACCTCTACAGATGCCAGCCTTGTGGGAAAGAAGAGTGGGCACCT
GAGGGAAGCCAGACCTGCTTCCCGCGCACTGTGGTGTTTTTGGCTTTGCGTGAGCACACCT
CTTGGGTGCTGCTGGCAGCTAACACGCTGCTGCTGCTGCTGCTGCTTGGGACTGCTGGCCT

GTTTGCCTGGCACCTAGACACCCCTGTGGTGAGGTCAGCAGGGGGCCGCCTGTGCTTTCTT
ATGCTGGGCTCCCTGGCAGCAGGTAGTGGCAGCCTCTATGGCTTCTTTGGGGAACCCACAA
GGCCTGCGTGCTTGCTACGCCAGGCCCTCTTTGCCCTTGGTTTCACCATCTTCCTGTCCTGC
CTGACAGTTCGCTCATTCCAACTAATCATCATCTTCAAGTTTTCCACCAAGGTACCTACATT
CTACCACGCCTGGGTCCAAAACCACGGTGCTGGCCTGTTTGTGATGATCAGCTCAGCGGCC
CAGCTGCTTATCTGTCTAACTTGGCTGGTGGTGTGGACCCCACTGCCTGCTAGGGAATACC
AGCGCTTCCCCCATCTGGTGATGCTTGAGTGCACAGAGACCAACTCCCTGGGCTTCATACT
GGCCTTCCTCTACAATGGCCTCCTCTCCATCAGTGCCTTTGCCTGCAGCTACCTGGGTAAG
GACTTGCCAGAGAACTACAACGAGGCCAAATGTGTCACCTTCAGCCTGCTCTTCAACTTCG
TGTCCTGGATCGCCTTCTTCACCACGGCCAGCGTCTACGACGGCAAGTACCTGCCTGCGGC
CAACATGATGGCTGGGCTGAGCAGCCTGAGCAGCGGCTTCGGTGGGTATTTTCTGCCTAAG
TGCTACGTGATCCTCTGCCGCCCAGACCTCAACAGCACAGAGCACTTCCAGGCCTCCATTC
AGGACTACACGAGGCGCTGCGGCTCCACCTGA (SEQ ID NO 1)

hT1R1 conceptual translation (SEQ ID NO 2)

MLLCTARLVGLQLLISCCWAFACHSTESSPDFTLPGDYLLAGLFPLHSGCLQVRHRPEVTLCDR
SCSFNEHGYHLFQAMRLGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQHHIE
LQGDLLHYSPTVLAVIGPDSTNRAATTAALLSPFLVPMISYAASSETLSVKRQYPSFLRTIPNDK
YQVETMVLLLQKFGWTWISLVGSSDDYGQLGVQALENQATGQGICIAFKDIMPFSAQVGDER
MQCLMRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKVWVASEAWALSRHITGVPGIQR
IGMVLGVAIQKRAVPGLKAFEEAYARADKKAPRPCHKGSWCSSNQLCRECQAFMAHTMPKL
KAFSMSSAYNAYRAVYAVAHGLHQLLGCASGACSRGRVYPWQLLEQIHKVHFLLHKDTVAF
NDNRDPLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLNINETKIQWHGKDNQVPKSVCSSDC
LEGHQRVVTGFHHCCFECVPCGAGTFLNKSDLYRCQPCGKEEWAPEGSQTCFPRTVVFLALRE
HTSWVLLAANTLLLLLLLGTAGLFAWHLDTPVVRSAGGRLCFLMLGSLAAGSGSLYGFFGEPT
RPACLLRQALFALGFTIFLSCLTVRSFQLIIIFKFSTKVPTFYHAWVQNHGAGLFVMISSAAQLLI
CLTWLVVWTPLPAREYQRFPHLVMLECTETNSLGFILAFLYNGLLSISAFACSYLGKDLPENYN
EAKCVTFSLLFNFVSWIAFFTTASVYDGKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCRPDL
NSTEHFQASIQDYTRRCGST (SEQ ID NO 2)

EXAMPLE 2 – hT1R2

The predicted cds of the human ortholog of a rat taste receptor, designated rT1R2, is provided below as SEQ ID NO 3. The conceptually translated hT1R2 sequences is also described herein as SEQ ID NO 4. According to the present invention, the first two coding exons of hT1R2 were identified within a PAC by Southern blot. Exon 1 was isolated within a BamHI/BglII fragment that was identified in the Southern experiment, and exon 2 was isolated within a PCR product

that spans exon 1 to exon 3. Comparison of the first two coding exons to the rT1R2 sequence established that the two exons encode the N-terminus of the human counterpart to rT1R2. For example, the pairwise amino acid identity between the hT1R2 N-terminal sequence coded by the two exons and corresponding regions of rT1R2 is approximately 72%, whereas the most related annotated sequence in public DNA sequence data banks is only approximately 48% identical to hT1R2.

hT1R2 predicted cds (SEQ ID NO 3)

ATGGGGCCCAGGGCAAAGACCATCTGCTCCCTGTTCTTCCTCCTATGGGTCCTGGCTGAGC
CGGCTGAGAACTCGGACTTCTACCTGCCTGGGGATTACCTCCTGGGTGGCCTCTTCTCCCT
CCATGCCAACATGAAGGGCATTGTTCACCTTAACTTCCTGCAGGTGCCCATGTGCAAGGAG
TATGAAGTGAAGGTGATAGGCTACAACCTCATGCAGGCCATGCGCTTCGCGGTGGAGGAG
ATCAACAATGACAGCAGCCTGCTGCCTGGTGTGCTGCTGGGCTATGAGATCGTGGATGTGT
GCTACATCTCCAACAATGTCCAGCCGGTGCTCTACTTCCTGGCACACGAGGACAACCTCCT
TCCCATCCAAGAGGACTACAGTAACTACATTTCCCGTGTGGTGGCTGTCATTGGCCCTGAC
AACTCCGAGTCTGTCATGACTGTGGCCAACTTCCTCTCCCTATTTCTCCTTCCACAGATCAC
CTACAGCGCCATCAGCGATGAGCTGCGAGACAAGGTGCGCTTCCCGGCTTTGCTGCGTACC
ACACCCAGCGCCGACCACCACGTCGAGGCCATGGTGCAGCTGATGCTGCACTTCCGCTGGA
ACTGGATCATTGTGCTGGTGAGCAGCGACACCTATGGCCGCGACAATGGCCAGCTGCTTG
GCGAGCGCGTGGCCCGGCGCGACATCTGCATCGCCTTCCAGGAGACGCTGCCCACACTGC
AGCCCAACCAGAACATGACGTCAGAGGAGCGCCAGCGCCTGGTGACCATTGTGGACAAGC
TGCAGCAGAGCACAGCGCGCGTCGTGGTCGTGTTCTCGCCCGACCTGACCCTGTACCACTT
CTTCAATGAGGTGCTGCGCCAGAACTTCACGGGCGCCGTGTGGATCGCCTCCGAGTCCTGG
GCCATCGACCCGGTCCTGCACAACCTCACGGAGCTGGGCCACTTGGGCACCTTCCTGGGCA
TCACCATCCAGAGCGTGCCCATCCCGGGCTTCAGTGAGTTCCGCGAGTGGGGCCCACAGGC
TGGGCCGCCACCCCTCAGCAGGACCAGCCAGAGCTATACCTGCAACCAGGAGTGCGACAA
CTGCCTGAACGCCACCTTGTCCTTCAACACCATTCTCAGGCTCTCTGGGGAGCGTGTCGTC
TACAGCGTGTACTCTGCGGTCTATGCTGTGGCCCATGCCCTGCACAGCCTCCTCGGCTGTG
ACAAAAGCACCTGCACCAAGAGGGTGGTCTACCCCTGGCAGCTGCTTGAGGAGATCTGGA
AGGTCAACTTCACTCTCCTGGACCACCAAATCTTCTTCGACCCGCAAGGGGACGTGGCTCT
GCACTTGGAGATTGTCCAGTGGCAATGGGACCGGAGCCAGAATCCCTTCCAGAGCGTCGC
CTCCTACTACCCCCTGCAGCGACAGCTGAAGAACATCCAAGACATCTCCTGGCACACCGTC
AACAACACGATCCCTATGTCCATGTGTTCCAAGAGGTGCCAGTCAGGGCAAAAGAAGAAG
CCTGTGGGCATCCACGTCTGCTGCTTCGAGTGCATCGACTGCCTTCCCGGCACCTTCCTCA
ACCACACTGAAGATGAATATGAATGCCAGGCCTGCCCGAATAACGAGTGGTCCTACCAGA
GTGAGACCTCCTGCTTCAAGCGGCAGCTGGTCTTCCTGGAATGGCATGAGGCACCCACCAT
CGCTGTGGCCCTGCTGGCCGCCCTGGGCTTCCTCAGCACCCTGGCCATCCTGGTGATATTC

TGGAGGCACTTCCAGACACCCATAGTTCGCTCGGCTGGGGGCCCCATGTGCTTCCTGATGC
TGACACTGCTGCTGGTGGCATACATGGTGGTCCCGGTGTACGTGGGGCCGCCCAAGGTCTC
CACCTGCCTCTGCCGCCAGGCCCTCTTTCCCCTCTGCTTCACAATTTGCATCTCCTGTATCG
CCGTGCGTTCTTTCCAGATCGTCTGCGCCTTCAAGATGGCCAGCCGCTTCCCACGCGCCTA
CAGCTACTGGGTCCGCTACCAGGGGCCCTACGTCTCTATGGCATTTATCACGGTACTCAAA
ATGGTCATTGTGGTAATTGGCATGCTGGCCACGGGCCTCAGTCCCACCACCCGTACTGACC
CCGATGACCCCAAGATCACAATTGTCTCCTGTAACCCCAACTACCGCAACAGCCTGCTGTT
CAACACCAGCCTGGACCTGCTGCTCTCAGTGGTGGGTTTCAGCTTCGCCTACATGGGCAAA
GAGCTGCCCACCAACTACAACGAGGCCAAGTTCATCACCCTCAGCATGACCTTCTATTTCA
CCTCATCCGTCTCCCTCTGCACCTTCATGTCTGCCTACAGCGGGGTGCTGGTCACCATCGTG
GACCTCTTGGTCACTGTGCTCAACCTCCTGGCCATCAGCCTGGGCTACTTCGGCCCCAAGT
GCTACATGATCCTCTTCTACCCGGAGCGCAACACGCCCGCCTACTTCAACAGCATGATCCA
GGGCTACACCATGAGGAGGGACTAG (SEQ ID NO. 3)

hT1R2 conceptual translation (SEQ ID NO 4)

MGPRAKTICSLFFLLWVLAEPAENSDFYLPGDYLLGGLFSLHANMKGIVHLNFLQVPMCKEYE
VKVIGYNLMQAMRFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDNLLPIQED
YSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELRDKVRFPALLRTTPSADHHVE
AMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIAFQETLPTLQPNQNMTSEERQ
RLVTIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIASESWAIDPVLHNLTELGH
LGTFLGITIQSVPIPGFSEFREWGPQAGPPPLSRTSQSYTCNQECDNCLNATLSFNTILRLSGERV
VYSVYSAVYAVAHALHSLLGCDKSTCTKRVVYPWQLLEEIWKVNFTLLDHQIFFDPQGDVAL
HLEIVQWQWDRSQNPFQSVASYYPLQRQLKNIQDISWHTVNNTIPMSMCSKRCQSGQKKKPV
GIHVCCFECIDCLPGTFLNHTEDEYECQACPNNEWSYQSETSCFKRQLVFLEWHEAPTIAVALL
AALGFLSTLAILVIFWRHFQTPIVRSAGGPMCFLMLTLLLVAYMVVPVYVGPPKVSTCLCRQA
LFPLCFTICISCIAVRSFQIVCAFKMASRFPRAYSYWVRYQGPYVSMAFITVLKMVIVVIGMLAT
GLSPTTRTDPDDPKITIVSCNPNYRNSLLFNTSLDLLLSVVGFSFAYMGKELPTNYNEAKFITLS
MTFYFTSSVSLCTFMSAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNS
MIQGYTMRRD (SEQ ID NO. 4)

EXAMPLE 3 – hT1R3

The predicted hT1R3 coding sequence is provided as SEQ ID NO 5 and the conceptual translation is provided as SEQ ID NO 6. An alternative form of hT1R3 with a single nucleic acid variation indicated in **bold** (designated hT1R3a) is also provided as SEQ ID NO. 7.

hT1R3 predicted cds (SEQ ID NO 5)

ATGCTGGGCCCTGCTGTCCTGGGCCTCAGCCTCTGGGCTCTCCTGCACCCTGGGACGGGGG
CCCCATTGTGCCTGTCACAGCAACTTAGGATGAAGGGGGACTACGTGCTGGGGGGGCTGT
TCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGCAGCCGGACACGGCCCAGCAGCCCTG
TGTGCACCAGGTTCTCCTCAAACGGCCTGCTCTGGGCACTGGCCATGAAAATGGCCGTGGA
GGAGATCAACAACAAGTCGGATCTGCTGCCCGGGCTGCGCCTGGGCTACGACCTCTTTGAT
ACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCCAGCCTCATGTTCCTGGCCAAGGCAGGC
AGCCGCGACATCGCCGCCTACTGCAACTACACGCAGTACCAGCCCCGTGTGCTGGCTGTCA
TCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGGCAAGTTCTTCAGCTTCTTCCTCAT
GCCCCAGGTCAGCTACGGTGCTAGCATGGAGCTGCTGAGCGCCCGGGAGACCTTCCCCTCC
TTCTTCCGCACCGTGCCCAGCGACCGTGTGCAGCTGACGGCCGCCGCGGAGCTGCTGCAGG
AGTTCGGCTGGAACTGGGTGGCCGCCCTGGGCAGCGACGACGAGTACGGCCGGCAGGGCC
TGAGCATCTTCTCGGCCCTGGCCGCGGCACGCGGCATCTGCATCGCGCACGAGGGCCTGGT
GCCGCTGCCCCGTGCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTGCACCAGGT
GAACCAGAGCAGCGTGCAGGTGGTGCTGCTGTTCGCCTCCGTGCACGCCGCCCACGCCCTC
TTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGGCCAGCGAGGCCTGG
CTGACCTCTGACCTGGTCATGGGGCTGCCCGGCATGGCCCAGATGGGCACGGTGCTTGGCT
TCCTCCAGAGGGGTGCCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACGCACCTGGCCCT
GGCCACCGACCCGGCCTTCTGCTCTGCCCTGGGCGAGAGGGAGCAGGGTCTGGAGGAGGA
CGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGCAGG
GCTAAATCACCACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTGGCCCAGGCCCTG
CACAACACTCTTCAGTGCAACGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGC
AGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGGCGGGCTGCCGCTGCGGTTCGA
CAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT
GCCCAGGCTCCACGACGTGGGCAGGTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGAT
CCGCTGGCACACGTCTGACAACCAGAAGCCCGTGTCCCGGTGCTCGCGGCAGTGCCAGGA
GGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGCTACGACTGTGTGGACTGCGA
GGCGGGCAGCTACCGGCAAAACCCAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGA
GTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCGCAGGTCTCGGTTCCTGGCATGGGGC
GAGCCGGCTGTGCTGCTGCTGCTCCTGCTGCTGAGCCTGGCGCTGGGCCTTGTGCTGGCTG
CTTTGGGGCTGTTCGTTCACCATCGGGACAGCCCACTGGTTCAGGCCTCGGGGGGGCCCCT
GGCCTGCTTTGGCCTGGTGTGCCTGGGCCTGGTCTGCCTCAGCGTCCTCCTGTTCCCTGGCC
AGCCCAGCCCTGCCCGATGCCTGGCCCAGCAGCCCTTGTCCCACCTCCCGCTCACGGGCTG
CCTGAGCACACTCTTCCTGCAGGCGGCCGAGATCTTCGTGGAGTCAGAACTGCCTCTGAGC
TGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGGCCTGGCTGGTGGTGCTGCTG
GCCATGCTGGTGGAGGTCGCACTGTGCACCTGGTACCTGGTGGCCTTCCCGCCGGAGGTGG
TGACGGACTGGCACATGCTGCCCACGGAGGCGCTGGTGCACTGCCGCACACGCTCCTGGG
TCAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTGGCCTTTCTCTGCTTCCTGGGCAC
TTTCCTGGTGCGGAGCCAGCCGGGCcGCTACAACCGTGCCCGTGGCCTCACCTTTGCCATG
CTGGCCTACTTCATCACCTGGGTCTCCTTTGTGCCCCTCCTGGCCAATGTGCAGGTGGTCCT

CAGGCCCGCCGTGCAGATGGGCGCCCTCCTGCTCTGTGTCCTGGGCATCCTGGCTGCCTTC
CACCTGCCCAGGTGTTACCTGCTCATGCGGCAGCCAGGGCTCAACACCCCCGAGTTCTTCC
TGGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAATGACGGGAACACAGGAAATCAGGGG
AAACATGAGTGA (SEQ ID NO 5)

<u>hT1R3 conceptual translation (SEQ ID NO 6)</u>

MLGPAVLGLSLWALLHPGTGAPLCLSQQLRMKGDYVLGGLFPLGEAEEAGLRSRTRPSSPVCT
RFSSNGLLWALAMKMAVEEINNKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKAGSRDI
AAYCNYTQYQPRVLAVIGPHSSELAMVTGKFFSFFLMPQVSYGASMELLSARETFPSFFRTVPS
DRVQLTAAAELLQEFGWNWVAALGSDDEYGRQGLSIFSALAAARGICIAHEGLVPLPRADDSR
LGKVQDVLHQVNQSSVQVVLLFASVHAAHALFNYSISSRLSPKVWVASEAWLTSDLVMGLPG
MAQMGTVLGFLQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQGLEEDVVGQRCPQCDCI
TLQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASGCPAQDPVKPWQLLENMYNLTFHV
GGLPLRFDSSGNVDMEYDLKLWVWQGSVPRLHDVGRFNGSLRTERLKIRWHTSDNQKPVSR
CSRQCQEGQVRRVKGFHSCCYDCVDCEAGSYRQNPDDIACTFCGQDEWSPERSTRCFRRRSRF
LAWGEPAVLLLLLLLSLALGLVLAALGLFVHHRDSPLVQASGGPLACFGLVCLGLVCLSVLLFP
GQPSPARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESELPLSWADRLSGCLRGPWAWLVVLLA
MLVEVALCTWYLVAFPPEVVTDWHMLPTEALVHCRTRSWVSFGLAHATNATLAFLCFLGTFL
VRSQPGCYNRARGLTFAMLAYFITWVSFVPLLANVQVVLRPAVQMGALLLCVLGILAAFHLPR
CYLLMRQPGLNTPEFFLGGGPGDAQGQNDGNTGNQGKHE (SEQ ID NO 6)

<u>HT1R3a predicted cds (SEQ ID NO 7)</u>

ATGCTGGGCCCTGCTGTCCTGGGCCTCAGCCTCTGGGCTCTCCTGCACCCTGGGACGGGG
CCCCATTGTGCCTGTCACAGCAACTTAGGATGAAGGGGGACTACGTGCTGGGGGGGCTGT
TCCCCCTGGGCGAGGCCGAGGAGGCTGGCCTCCGCAGCCGGACACGGCCCAGCAGCCCTG
TGTGCACCAGGTTCTCCTCAAACGGCCTGCTCTGGGCACTGGCCATGAAAATGGCCGTGGA
GGAGATCAACAACAAGTCGGATCTGCTGCCCGGGCTGCGCCTGGGCTACGACCTCTTTGAT
ACGTGCTCGGAGCCTGTGGTGGCCATGAAGCCCAGCCTCATGTTCCTGGCCAAGGCAGGC
AGCCGCGACATCGCCGCCTACTGCAACTACACGCAGTACCAGCCCCGTGTGCTGGCTGTCA
TCGGGCCCCACTCGTCAGAGCTCGCCATGGTCACCGGCAAGTTCTTCAGCTTCTTCCTCAT
GCCCCAGGTCAGCTACGGTGCTAGCATGGAGCTGCTGAGCGCCCGGGAGACCTTCCCCTCC
TTCTTCCGCACCGTGCCCAGCGACCGTGTGCAGCTGACGGCCGCCGCGGAGCTGCTGCAGG
AGTTCGGCTGGAACTGGGTGGCCGCCCTGGGCAGCGACGACGAGTACGGCCGGCAGGGCC
TGAGCATCTTCTCGGCCCTGGCCGCGGCACGCGGCATCTGCATCGCGCACGAGGGCCTGGT
GCCGCTGCCCCGTGCCGATGACTCGCGGCTGGGGAAGGTGCAGGACGTCCTGCACCAGGT
GAACCAGAGCAGCGTGCAGGTGGTGCTGCTGTTCGCCTCCGTGCACGCCGCCCACGCCCTC
TTCAACTACAGCATCAGCAGCAGGCTCTCGCCCAAGGTGTGGGTGGCCAGCGAGGCCTGG
CTGACCTCTGACCTGGTCATGGGGCTGCCCGGCATGGCCCAGATGGGCACGGTGCTTGGCT
TCCTCCAGAGGGGTGCCCAGCTGCACGAGTTCCCCCAGTACGTGAAGACGCACCTGGCCCT

GGCCACCGACCCGGCCTTCTGCTCTGCCCTGGGCGAGAGGGAGCAGGGTCTGGAGGAGGA
CGTGGTGGGCCAGCGCTGCCCGCAGTGTGACTGCATCACGCTGCAGAACGTGAGCGCAGG
GCTAAATCACCACCAGACGTTCTCTGTCTACGCAGCTGTGTATAGCGTGGCCCAGGCCCTG
CACAACACTCTTCAGTGCAACGCCTCAGGCTGCCCCGCGCAGGACCCCGTGAAGCCCTGGC
AGCTCCTGGAGAACATGTACAACCTGACCTTCCACGTGGGCGGGCTGCCGCTGCGGTTCGA
CAGCAGCGGAAACGTGGACATGGAGTACGACCTGAAGCTGTGGGTGTGGCAGGGCTCAGT
GCCCAGGCTCCACGACGTGGGCAGGTTCAACGGCAGCCTCAGGACAGAGCGCCTGAAGAT
CCGCTGGCACACGTCTGACAACCAGAAGCCCGTGTCCCGGTGCTCGCGGCAGTGCCAGGA
GGGCCAGGTGCGCCGGGTCAAGGGGTTCCACTCCTGCTGCTACGACTGTGTGGACTGCGA
GGCGGGCAGCTACCGGCAAAACCCAGACGACATCGCCTGCACCTTTTGTGGCCAGGATGA
GTGGTCCCCGGAGCGAAGCACACGCTGCTTCCGCCGCAGGTCTCGGTTCCTGGCATGGGGC
GAGCCGGCTGTGCTGCTGCTGCTCCTGCTGCTGAGCCTGGCGCTGGGCCTTGTGCTGGCTG
CTTTGGGGCTGTTCGTTCACCATCGGGACAGCCCACTGGTTCAGGCCTCGGGGGGGCCCCT
GGCCTGCTTTGGCCTGGTGTGCCTGGGCCTGGTCTGCCTCAGCGTCCTCCTGTTCCCTGGCC
AGCCCAGCCCTGCCCGATGCCTGGCCCAGCAGCCCTTGTCCCACCTCCCGCTCACGGGCTG
CCTGAGCACACTCTTCCTGCAGGCGGCCGAGATCTTCGTGGAGTCAGAACTGCCTCTGAGC
TGGGCAGACCGGCTGAGTGGCTGCCTGCGGGGGCCCTGGGCCTGGCTGGTGGTGCTGCTG
GCCATGCTGGTGGAGGTCGCACTGTGCACCTGGTACCTGGTGGCCTTCCCGCCGGAGGTGG
TGACGGACTGGCACATGCTGCCCACGGAGGCGCTGGTGCACTGCCGCACACGCTCCTGGG
TCAGCTTCGGCCTAGCGCACGCCACCAATGCCACGCTGGCCTTTCTCTGCTTCCTGGGCAC
TTTCCTGGTGCGGAGCCAGCCGGGCCGCTACAACCGTGCCCGTGGCCTCACCTTTGCCATG
CTGGCCTACTTCATCACCTGGGTCTCCTTTGTGCCCCTCCTGGCCAATGTGCAGGTGGTCCT
CAGGCCCGCCGTGCAGATGGGCGCCCTCCTGCTCTGTGTCCTGGGCATCCTGGCTGCCTTC
CACCTGCCCAGGTGTTACCTGCTCATGCGGCAGCCAGGGCTCAACACCCCCGAGTTCTTCC
TGGGAGGGGGCCCTGGGGATGCCCAAGGCCAGAATGACGGGAACACAGGAAATCAGGGG
AAACATGAGTGA (SEQ ID NO 7)

Example 4 – PDZIP as an Export Sequence

The six residue PDZIP sequence (SEQ ID NO 10) was fused to the C-terminus of the orphan GPCR hT1R2 and transfected into an HEK-293 host cell. The surface expression of hT1R2 was then monitored using immunofluorescence and FACS scanning data. As demonstrated in Figure 1, the inclusion of the PDZIP sequence acted as a translocation domain and increased the surface expression of hT1R2-PDZIP relative to hT1R2.

PKZIP Sequence (SEQ ID NO 10)

SVSTVV (SEQ ID NO 10)

More specifically, Figure 1A shows an immunofluorescence staining of Myc-tagged hT1R2 and demonstrated that PDZIP significantly increases the amount of hT1R2 protein on the plasma membrane. Further, Figure 1B shows FACS analysis data demonstrating the same result - Myc-tagged hT1R2 in indicated in the dotted line and Myc-tagged hT1R2-PDZIP is indicated in the solid line.

Example 5 – Co-Expression of hT1R2 and hT1R3 in Taste Tissue

cDNA-specific amplification products were amplified from cDNA prepared from resected human circumvallate papillae and run on a gel with genomic DNA obtained from human tongue epithelium. As shown in Figure 3, hT1R2 and hT1R3 are co-expressed in taste tissue

Example 6 – hT1R2/hT1R3 Heterodimeric Complex

HEK-293 cells stably transfected with Gα15 were transfected with hT1R2, hT1R3, or a combination thereof, both with and without PDZIP. The response of the various transfected cells to a number of sweet stimuli were then monitored by calcium-imaging. Figure 2 shows the calcium-imaging data demonstrating that hT1R2 and hT1R3 are both required to trigger a response to the sweet stimuli. Thus, it was unexpectedly discovered that the response to sweet stimuli is dependent on the presence of both hT1R2 and hT1R3. Neither receptor alone resulted in any significant response to the stimuli.

More particularly, Figure 2A shows untransfected Gα15 stable host cells in HBS buffer, Figure 2B shows hT1R2-PDZIP transfected Gα15 stable host cells in sweetener pool no. 5 (saccharin, sodium cyclamate, Acesulfame K, and Aspartame – 20 mM each in HBS buffer), Figure 2C shows hT1R3-PDZIP transfected Gα15 stable host cells in sweetener pool no. 5, and Figure 2D shows hT1R2-PDZIP/hT1R3-PDZIP co-transfected Gα15 stable host cells in sweetener pool no. 5. Further, Figures 2E-2H show dose-dependent response of hT1R2/hT1R3 co-transfected Gα15 stable host cells to sucrose – E: 0 mM in HBS buffer; F: 30 mM; G: 60 mM; and H: 250 mM. Figures 2I-2L shown the responses of hT1R2/hT1R3 co-transfected Gα15 stable host cells to individual sweeteners – I: Aspartame (1.5 mM); J: Acesulfame K (1 mM); K:

Neotame (20 mM); L: Sodium cyclamate (20 mM). As demonstrated by the calcium-images of Figure 2, hT1R2 and hT1R3 are both required for the activities triggered by the sweet stimuli.

Example 7

hT1R2 and hT1R3 Function in Combination and Couple to $G_{\square 15}$

To demonstrate that hT1R2 and hT1R3 function in combination, we transfected the receptors individually and in combination into HEK-G15 cells. We have determined that T1R2/T1R3 activity is not enhanced by incorporation of PDZIP into the receptors; consequently, unmodified receptors are used in the assays described herein. Transfected cells were loaded with Fluo-4, and their responses to a mixture of sweet taste stimuli (Saccharin, Cyclamate, AcesulfameK, Aspartame, 10mM each) were determined by fluorescence microscopy. Responses of imaged fields of transfected cells are shown in Fig. 4. Responses to the sweetener pool were only detected in cells contransfected with hT1R2 and hT1R3 (panel C), but not with hT1R2 (panel A) or hT1R3 (panel B) alone. The G-protein dependence of T1R2/T1R3 activity was similarly determined by cotransfection of the T1Rs and different G proteins into HEK-293T cells, which unlike HEK-G15 cells do not express $G_{\square 15}$. In the panels below, sucrose (120 mM) responses were detected in cells that transiently express $G_{\square 15}$ (panel E), but not Gq (panel D). Thus, T1R2 and T1R3 together are activated by sweet taste stimuli, and they couple to $G_{\square 15}$, thereby allowing their activity to be determined by fluorescence-based whole-cell assay.

Example 8

Quantitative Assay of the Human T1R2/T1R3 Sweet Receptor

We have developed a method to quantitate hT1R2/hT1R3 activity that can be used, for example, to predict the potency of new candidate sweeteners. In this quantitative assay, HEK-G15 cells that are transiently transfected with hT1R2 and hT1R3 are loaded with the calcium dye Fluo-4, and their responses to sweeteners are observed with a fluorescent microscope. Dose responses are obtained by quantitation of the number of responding cells. Fig. 5 presents dose responses for sucrose, tryptophan, and five commercially important artificial sweeteners. The dose responses obtained argue compellingly that T1R2/T1R3 is the human sweet taste receptor because the rank order and threshold values obtained in this assay mirrors values for human sweet taste.

Example 9

As an example of how such an assay can be adapted to a high-throughput screening format, HEK-G15 cells that are transiently transfected with hT1R2 and hT1R3 were loaded with the calcium dye Fluo-4, and their responses to sweeteners were determined using an automated fluorescence plate reader. Fig. 6 presents cyclamate (12.5 mM) responses measured for cells expressing hT1R2/hT1R3 (K19-22) and for cells expressing only hT1R3 (J19-22). As noted above, responses to this stimulus only occur in cells expressing T1R2 and T1R3 in combination.

Example 10

Possible Function of T1R1

If the human sweet receptor is composed of hT1R2 and hT1R3 then what does hT1R1 do? Some of the recent T1R3 papers suggest that, although T1R1 and T1R2 are predominantly expressed in nonoverlapping regions of the oral cavity, both T1Rs are coexpressed with T1R3. Thus, we hypothesize that T1R1, like T1R2, may function in combination with T1R3 as a taste receptor. The specificity of the T1R1 or

T1R1/T1R3 receptor can only be guessed at present. It is widely believed, however, that taste buds throughout the oral cavity - even those that do not express T1R2 - are responsive to sweet taste stimuli. Thus, T1R1 or T1R1/T1R3 may function, like T1R2/T1R3, as a sweet taste receptor that is functionally similar to T1R2/T1R3. Alternatively, T1R1 or T1R1/T1R3 may function as a sweet receptor that is complementary to T1R2/T1R3, recognizing ligands such as glucose, alanine, and glycine that do not appear to activate T1R2/T1R3. One further compelling hypothesis is that T1R1 or T1R1/T1R3 recognizes glutamate and functions as the umami receptor. Such a possibility is hinted at by the observation that rodents may not discriminate between sweet taste stimuli and glutamate, and by the curious sequence relationship of T1R1 to the metabotropic glutamate receptors. Fig. 7 depicts the glutamate binding site in the X-ray crystal structure of mGluR1 (Kunishima et al., Nature 407, 971-977 (200)) with glutamate-binding residues that are conserved between mGluR1 and T1R1 in space-filling detail. It appears that the alpha-amino acid-binding determinants of mGluR1 may also be present in T1R1; thus, T1R1 may recognize the umami taste stimulus glutamate, or sweet-tasting amino acids such as alanine and glycine.

While the foregoing detailed description has described several embodiments of the present invention, it is to be understood that the above description is illustrative only and not limiting of the disclosed invention. The invention is to be limited only by the claims which follow.